

Figure 1

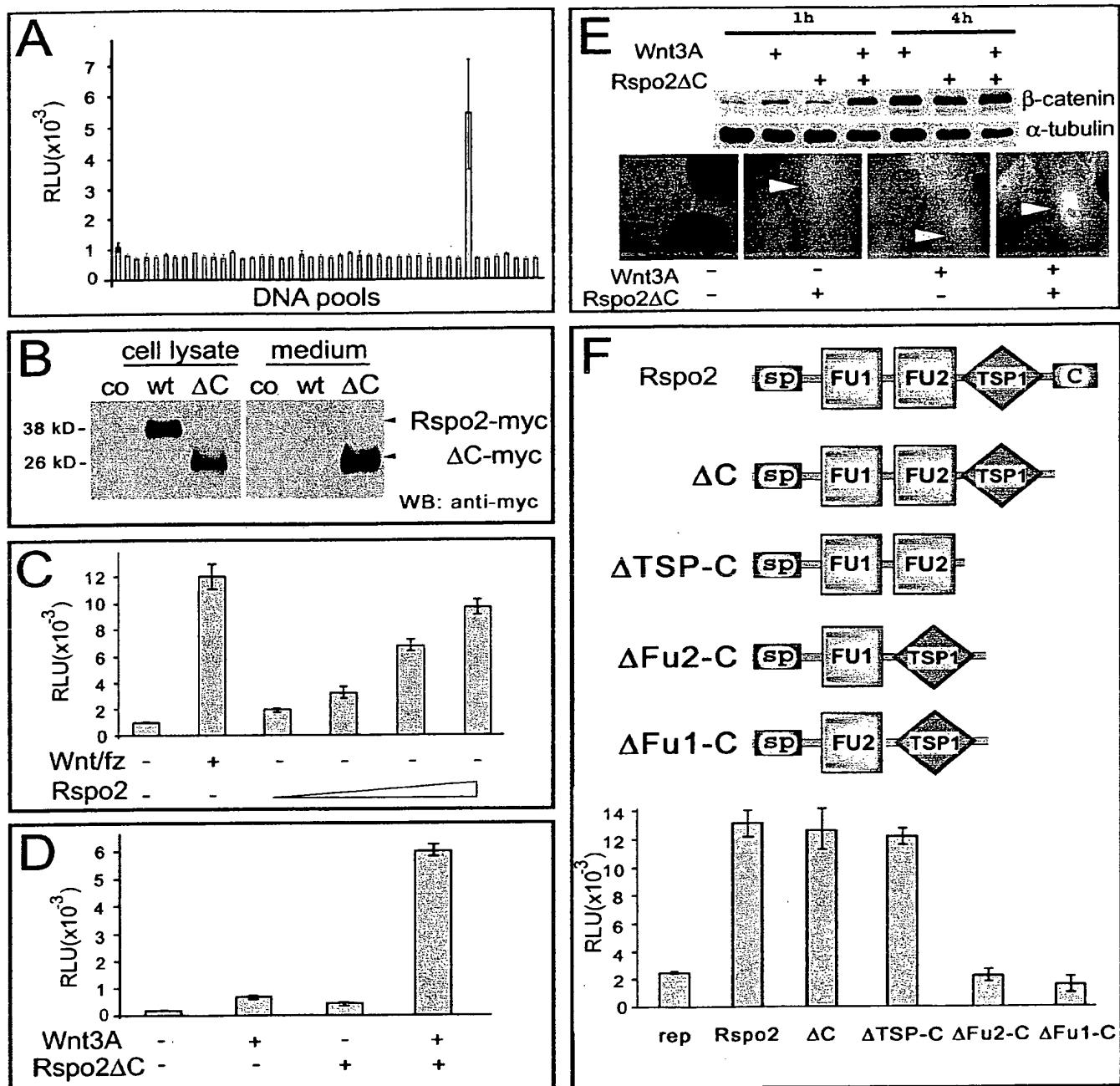


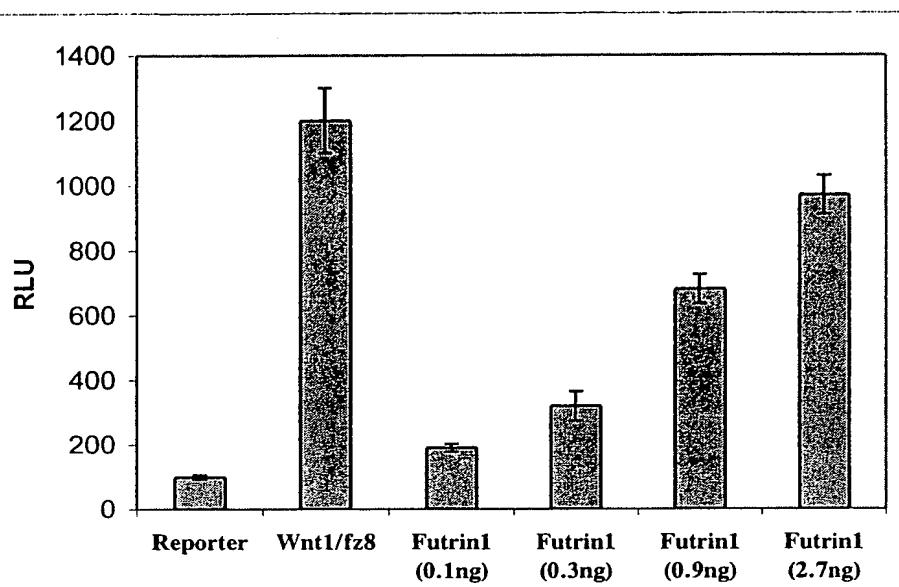
Figure 2

Figure 3

hFut1	161	MDFRLFSFALLILNCMDYSHCQ.GNRWRRSKRASYYVSNPICKG.CESCSKEDNGCSRCOOQ
hFut2	171	MELRLISWLFILNFMWYIIGSONASRGRORRWHPNVSQCGGATCSEYNGCLSKCKP
hFut3	1851	MRLGLCVVALVSWTHLTLISR.GIKGAKRORRISAEGSQACAKGCELCSEVNGCLKCSPK
hFut4	1881	MRAPLCLLVAHAVDMLALNR.....RKKQWYGTGCGNCCTG.CRICSEENGCSSTCQQR
hFut1	59	LEFFFLRREGMRQYGECLHSSCPSSGYMGERAPDMNRCAR.....CRIENC
hFut2	61	LEFFALERIGW30TGVCLSSCPSSGYMTRYPDINCTK.....CKAD.C
hFut3	60	LEFFLERINDRQVGVCLPSCPYPGYEDARNPDMMNCINSAVPAALGQQGPALHVECKIEHC
hFut4	54	LEFFLERREGERQYGRCLHDCCPPGYPEGIRGQEVNNRCKK.....CGAT.C
hFut1	102	DISCFPSKDFCTKCKVGFYLHGRSFDECPEGFAPLEETMECEVG.[CEVGHWSSEWGTCSRN
hFut2	103	DISCFENKNFCTKCKSGFYLHGRCLDNCPLEGLEANHTEMECVSIVHCEVSEMWNPWSPCCKK
hFut3	120	DISCFSENFCCTKCKEGLYLYHGRCPYAPCEGSSAANGTMECSSPAQCEMSEWSPWGPCCKK
hFut4	96	DISCFPSQDFCIECKRQFYLYKGKCLPTCPGELAHONTRECQGE.[CEVGPWGGWSPCFFEN
hFut1	160	NETTCGFKWQGLETRTRQIYKPKDTIPCPPTIAESRECKMTMRHCPGCKRE...PKANKEKR
hFut2	163	GKTCCGFKRGTETRVRLEIIOHPSAKENLCPPTNEFRECTVORKKQKGERG...KKGREK
hFut3	180	QQLCCGFERGSEERTTRRWHAPVSDHAACSDTEKEFRECTVRRVPCPEGOKR...EKGGQGR
hFut4	154	GKTCCGSAWGLEERVREAGFAGHEEAATCQVLSERSKCPHQ.R.PCP.GERSPGOKKGREKDR
hFut1	217	NKK.K...KRLKLIERAQEGHSVFTADRANQ-----
hFut2	220	RKKPNKGESKEAEPDSKSLESSKEPEORENKQQQKKRKYQDKQKSVSVSTVH
hFut3	237	REN....ANRNLAERESKEAGAGS.RRRKGQQQQQQGTVGPLTSAGPA-----
hFut4	212	RPN....KDRKLDRLD-----

Figure 4

A



B

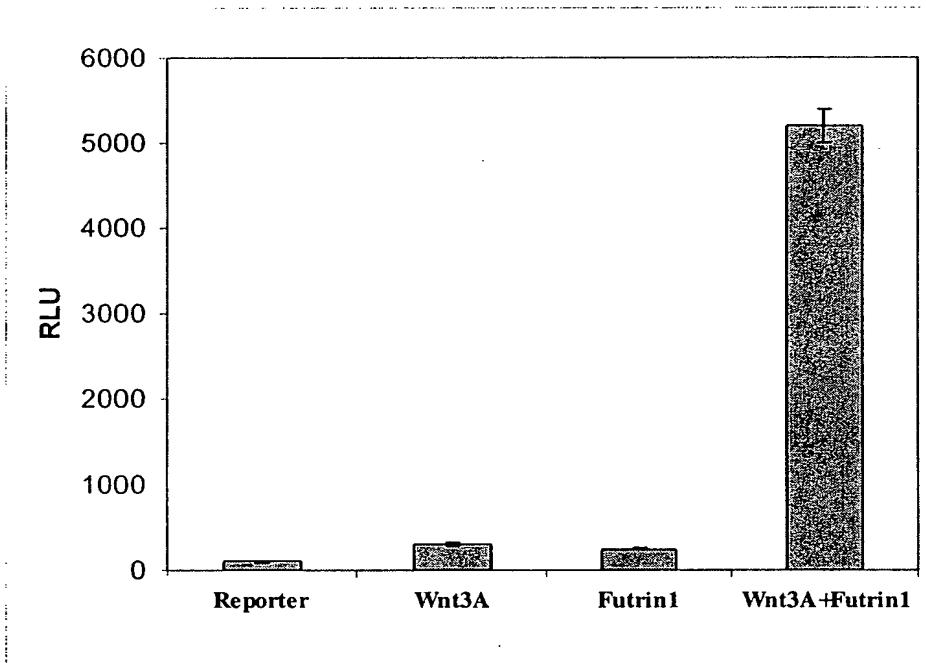


Figure 5

A

hR-spondin1 151 MRLGLCVVALVEWSWTHLTISSR. CIKGKROARRSAEGSQACAKGCEL CSEVNGCLKCSPK
 hR-spondin2 161 MQFLFLFSFALIILNCMDYSHCQ. GNRWRRSKRASYVSNPICKG. CESCSDKDNGCSRCCQOK
 hR-spondin3 171 MHLRLISWLFTILNFMELYIGSQNNSRGRQRHMHPNVSQGCQGGCATCSDYNGCLSCKPR
 hR-spondin4 181 MRAPLCLLLEVAHAVDMLALNR. RKKQVGTGEGGNCTG. CTCICSEENGESTCQOR

signal peptide

furin-like domain 1

hR-spondin1 60 LFIILLERNDTRQVGVCLPSCPAGYEDARNPDMNACI. CKIEHCEAACFSHNFTKCKEGLY
 hR-spondin2 59 LFFFLLRREGMRQYGECLHSCPSGYXGHRAPDMNRCARCRRIENCSCKSKDFCTKCKVGFY
 hR-spondin3 61 LFFAALERIGMKQIGVCLSSCPGSGYHGTTRYPDINKCTKCKAD. CDTACFNKNFTKCKSGFY
 hR-spondin4 54 LFLFLTRREGTRQYGKCLHDCEPAGYEGIRGQEVNRCKKKGAT. CESCFSQDFCIRCKRQFY

furin-like domain 2

hR-spondin1 119 LHKGRRCYPACPEGSSAANGTMECSSPAQCEMSSEWSPWGPCKKKQOLCGFRRGSEERTRRV
 hR-spondin2 119 LHRGRSFDECPDGFAFPLEETMECVEG. . . . CEVGHWSEWGTCSRNNRNTCGFKWGLETRTRQI
 hR-spondin3 120 LHLGKCLDNCPFEGLEANNHTMECVSIVHCEVSEWNPWSPCTKKGKTCGFKRGCTETRVREI
 hR-spondin4 113 LYKGKCLPTCPGTLAHQNTRECQGE. . . . CEEGPWGGWSPCTHNGKTCGSAWGLESRVREA

thrombospondin type 1 domain

hR-spondin1 180 EHAPVGDHAAACSDTKETTRRCTVRRVPCPEGQKR. . . . RKGGOGRREN. . . . ANRNLA
 hR-spondin2 160 VKKPVKDTIPCPPTIAESRCKMTMRHCPGGKRT. . . . EKAKERKRNKK. . . . KRKLIERA
 hR-spondin3 163 IOHPSAKGNLCPPTNETRKCTVQRKCKQKGERG. . . . KKGREKRRKPKPNKGESKEATPDSK
 hR-spondin4 154 GRAGHEEAATCQVLSESRKCPIOR. PCP. GERSPGQKKGRKDRRP. . . . KDRKLDRRL

B

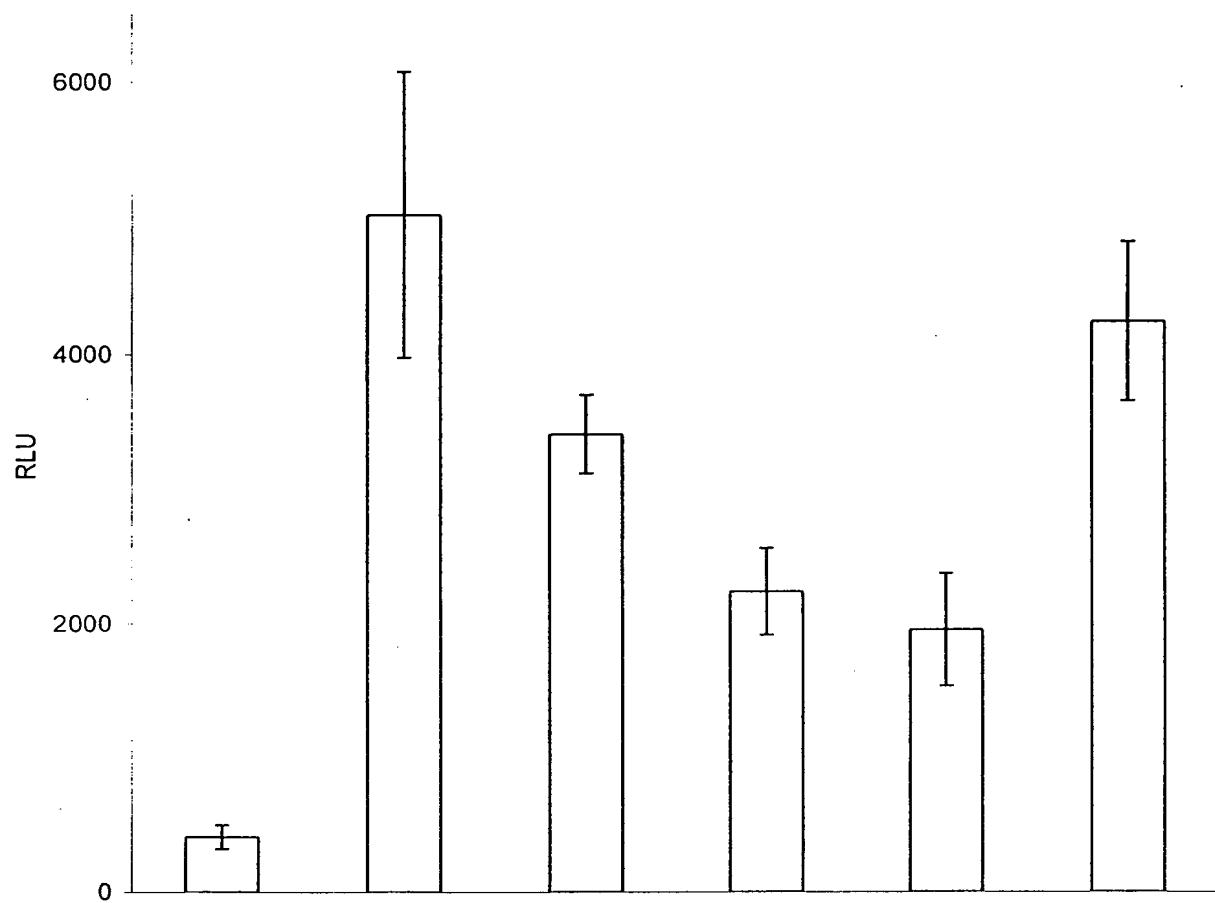
hRspo2	39.9			
hRspo3	43.7	45.9		
hRspo4	40.3	43.9	41.2	
	hRspo1	hRspo2	hRspo3	

C

mRspo2	40.5	95.5	44.2	44.8
XRspo2	40.8	83.5	43.8	42.2
	hRspo1	hRspo2	hRspo3	hRspo4

Figure 6

7117



pSuper Non.	+	+				
() pSuper hFut1			+		+	+
pSuper hFut2				+	+	+
Wnt3A med.	-	+	+	+	+	+
mFut1						+

Figure 7

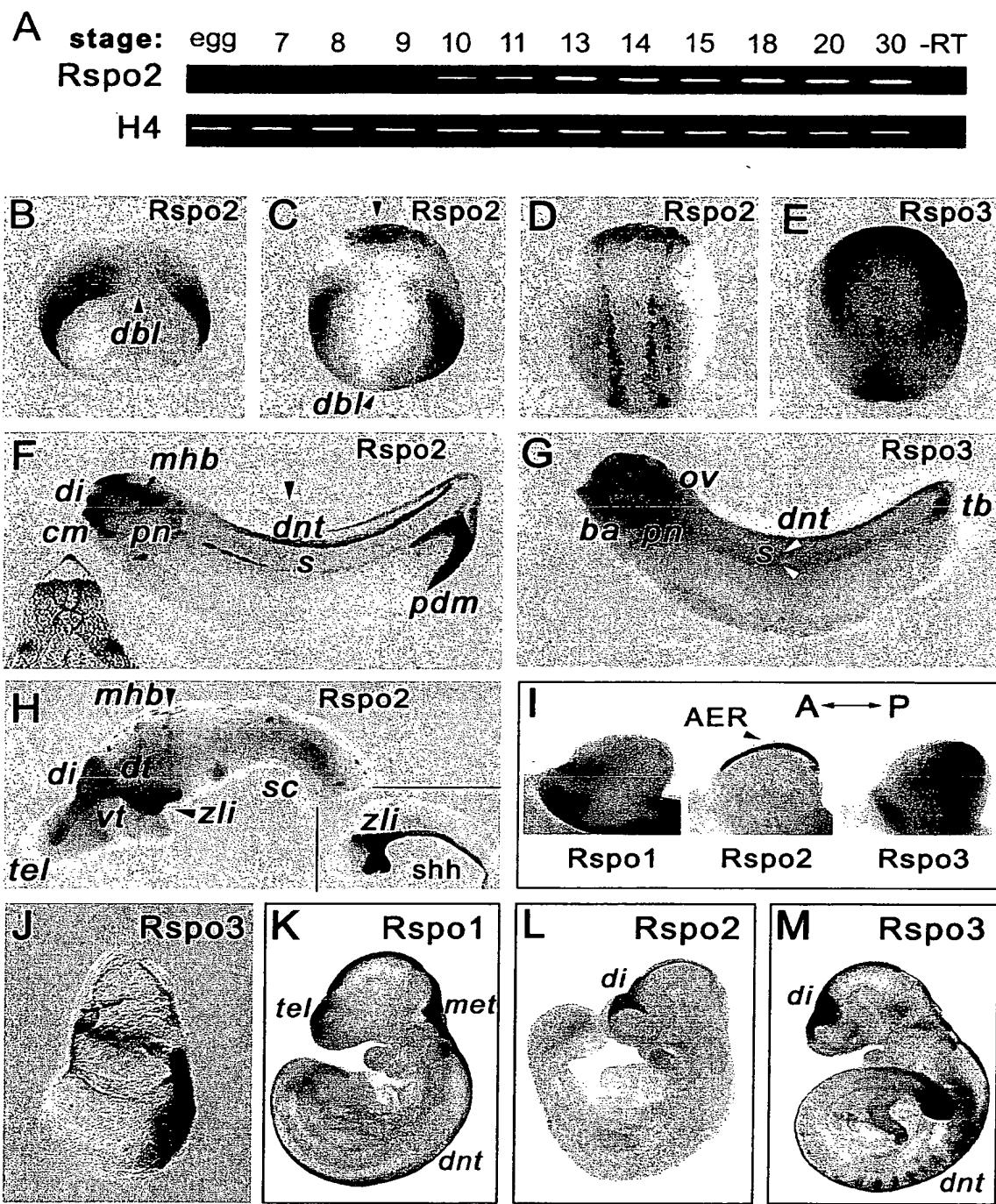


Figure 8

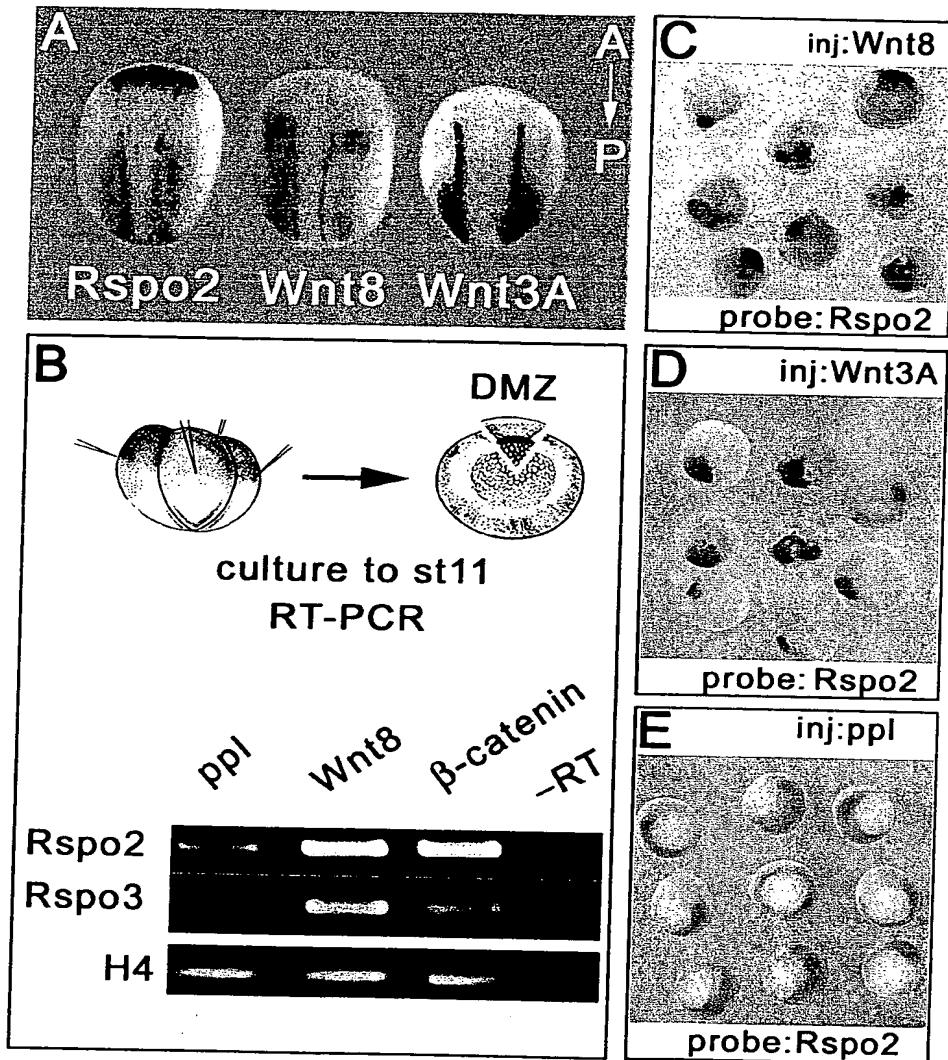


Figure 9

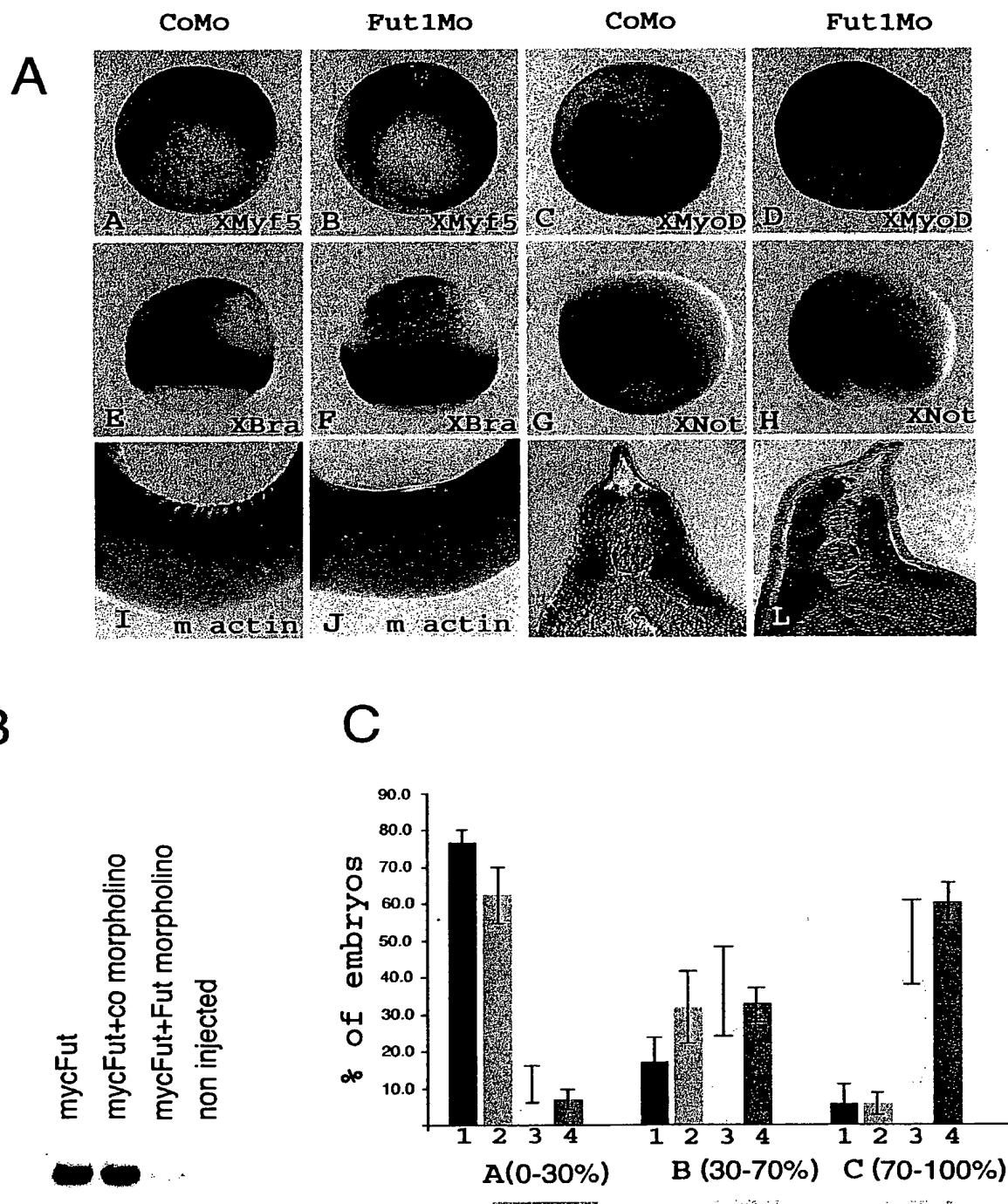


Figure 10

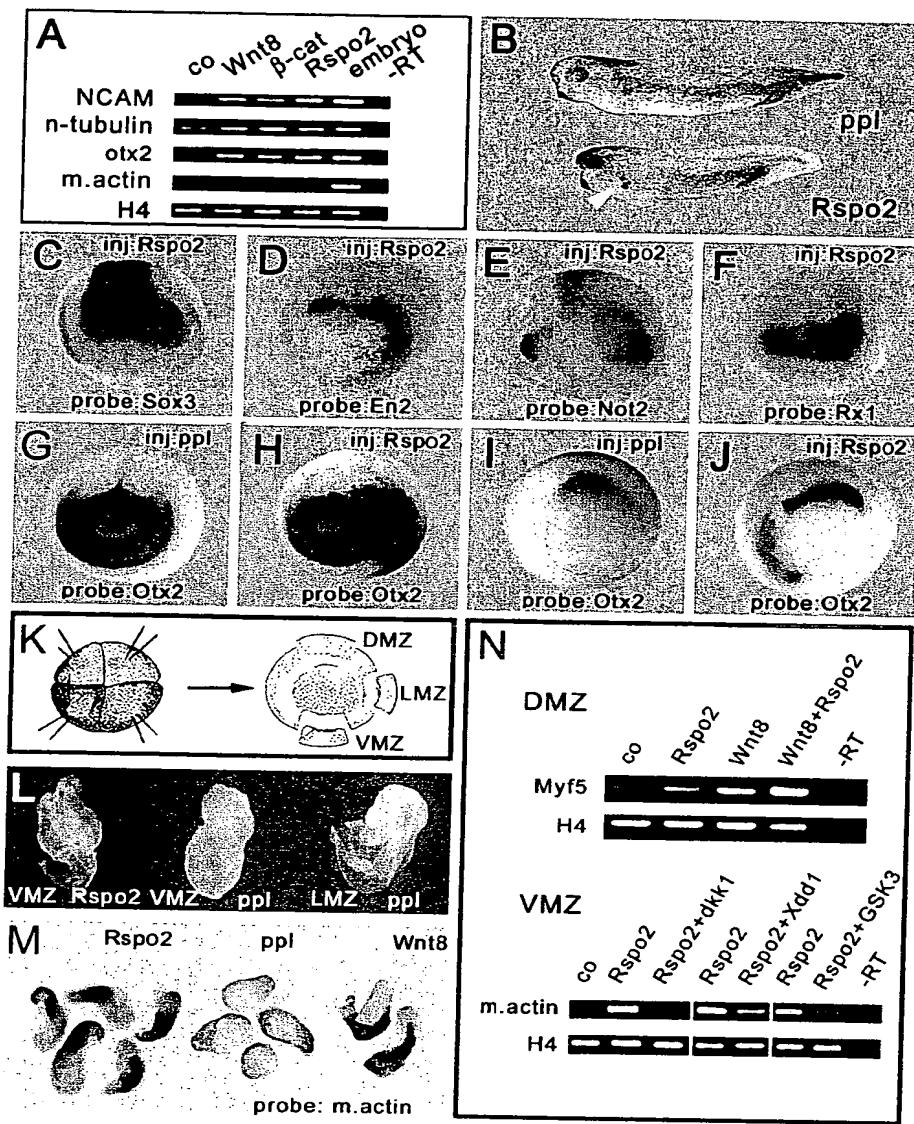


Figure 11

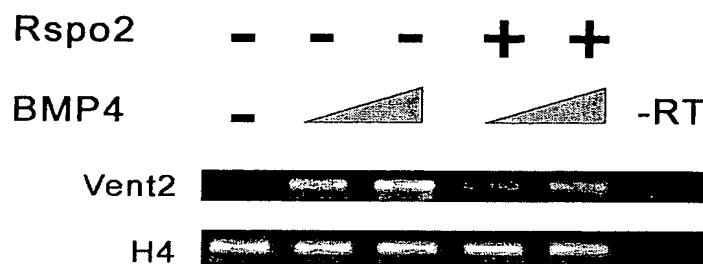
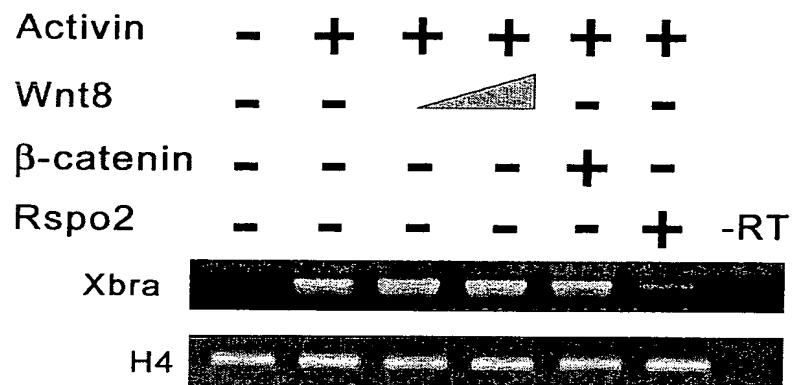
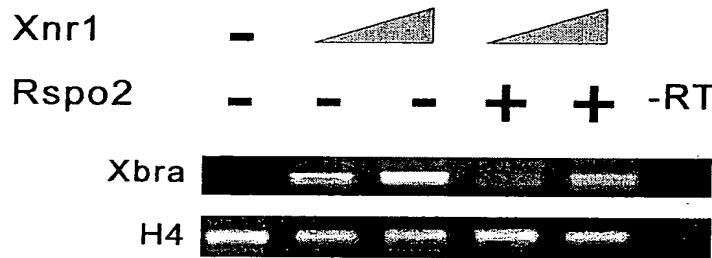
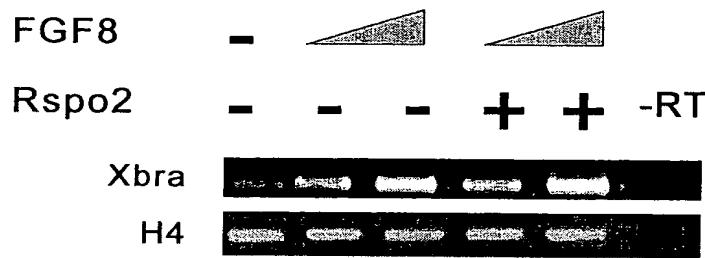
A**B****C****D**

Figure 12

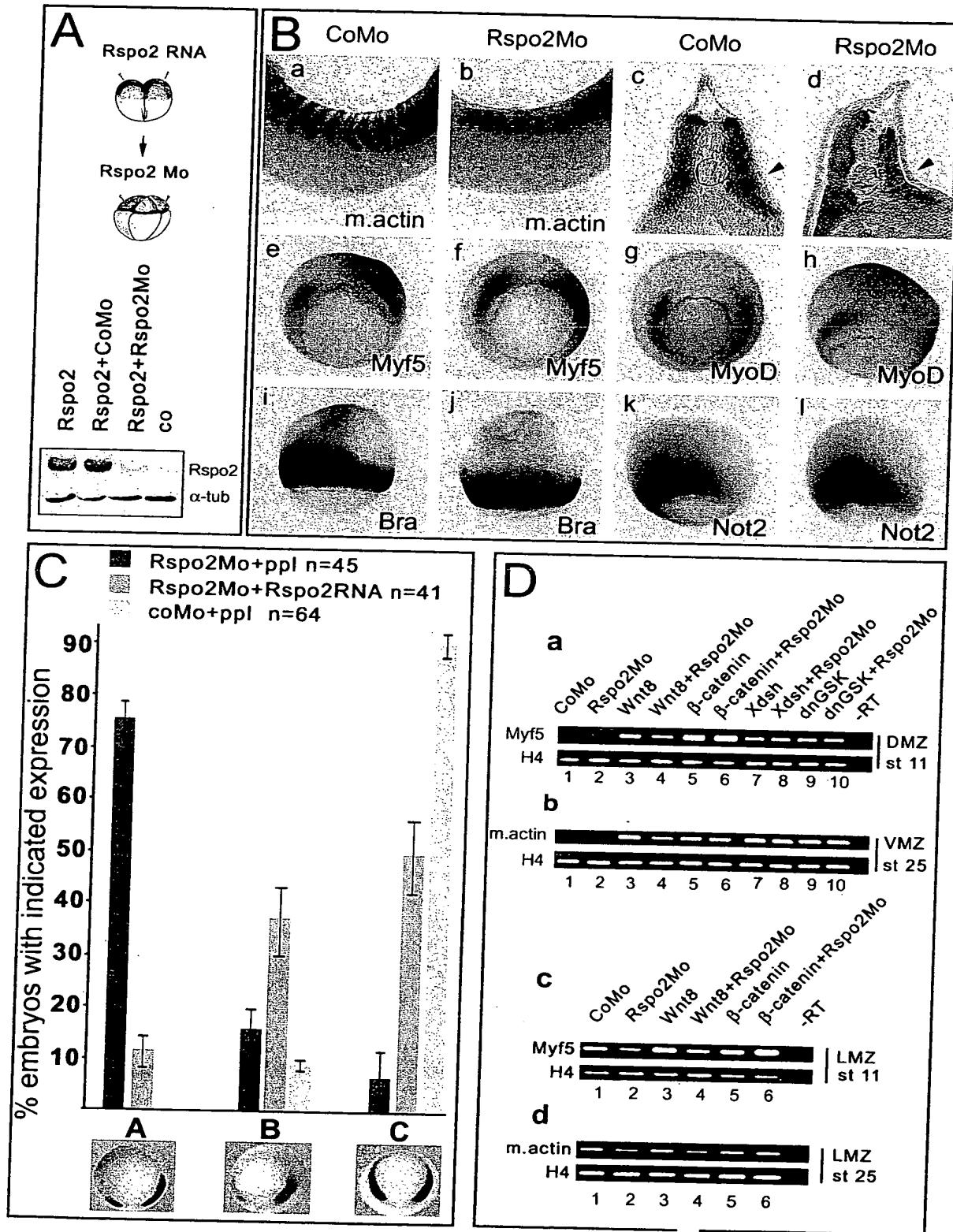


Figure 13

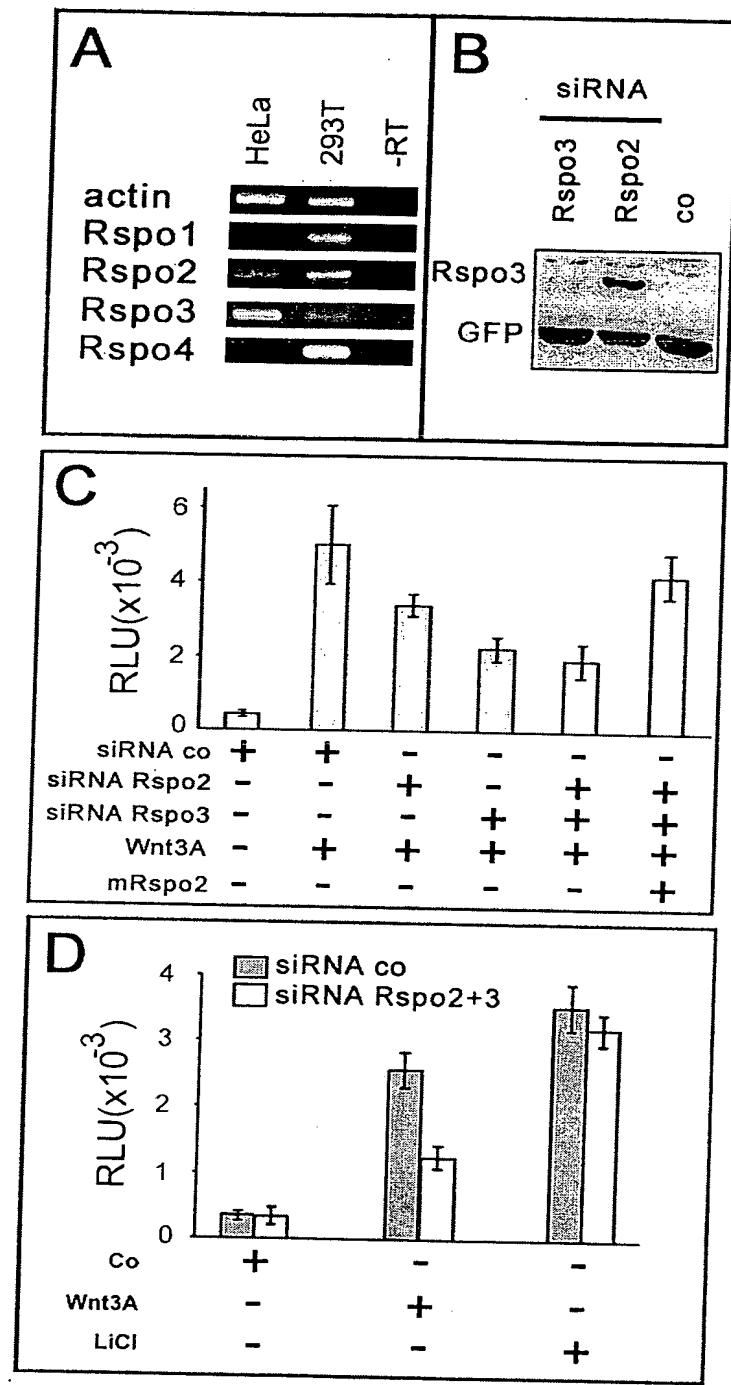
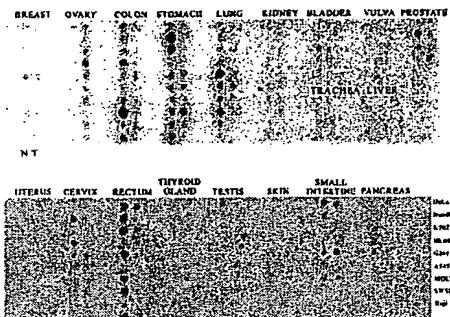
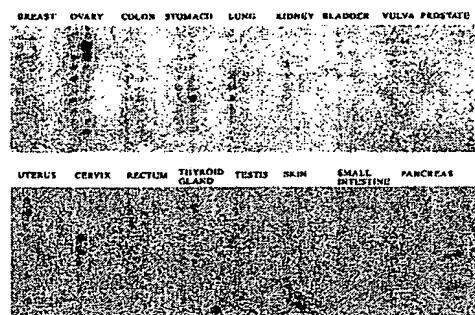
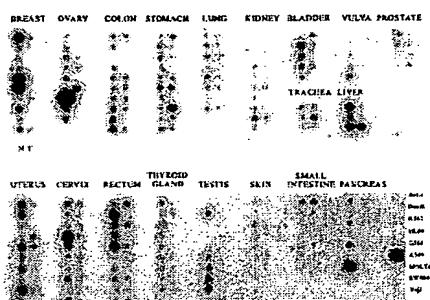
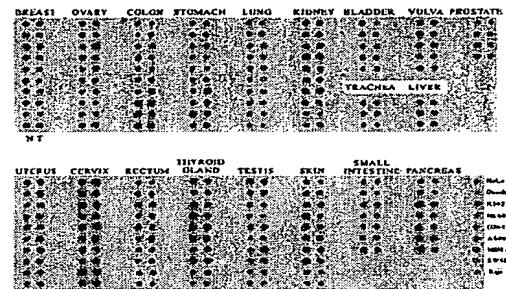


Figure 14

hFutrin1**hFutrin3****hFutrin2****Ubiquitin****hFutrin4****Figure 15**

16/17

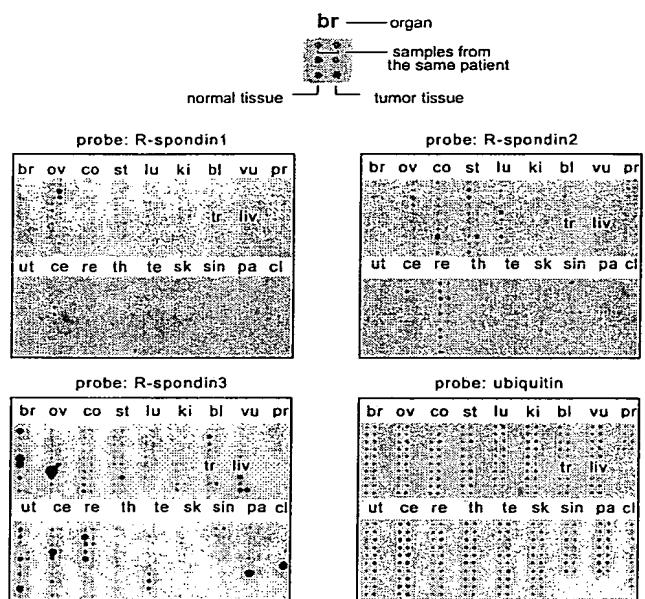


Figure 16

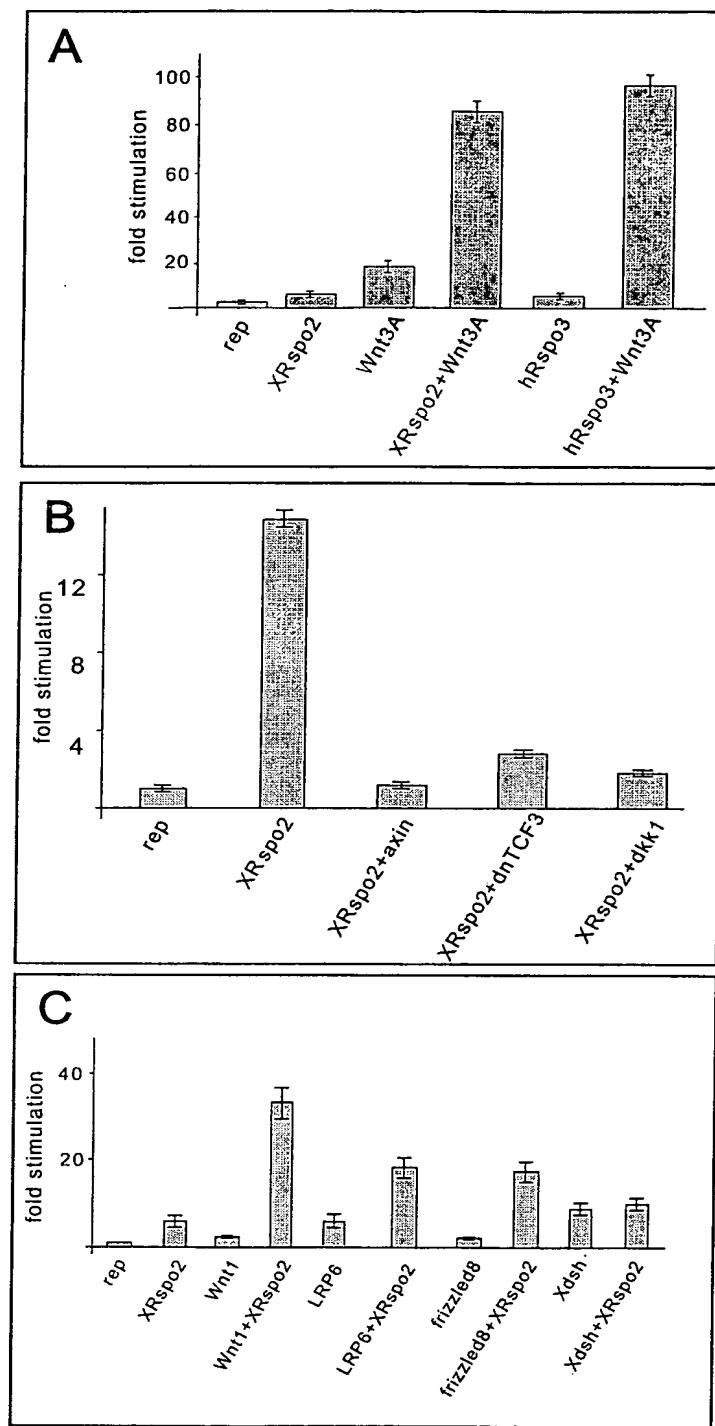


Figure 17

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